OBM	PTO-	1449	(Modified	١١

LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE **STATEMENT**

ATTY. DOCKET NO. 24737-1906B

SERIAL NO. 09/704,362

APPLICANT

Ramnarayan et al.

FILING DATE November 1, 2000

GROUP 1631

AUG 1 4 2002

U.S. PATENT DOCUMENTS

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EXAMINER INITIAL			D	ocuv	IENT N	NUMB	ER		DATE	NAME	CLASS	CLASS	1609/2999 DATE
193	AA	5	3	1	7	0	9	7	05/31/94	Miller et al.	536	24.31	10/07/91
7 183	AB	5	4	9	5	4	2	3	02/27/96	DeLisi <i>et al</i> .	·364	496	10/25/93
165	AC	5	5	9	3	9	5	9	01/14/97	Miller et al.	514	8	10/14/93
	AD	5	6	2	4	8	1	7	04/29/97	Miller et al.	435	69.1	04/28/94
X 65	ΑE	5	6	9	9	2	6	8	12/16/97	Schmidt	-364	496	06/07/95
25	AF	5	9	6	8	7	3	7	10/19/99	Ali-Osman et al.	435	-6-	11/12/96
100	AG	5	9	7	8	7	4	0	11/02/99	Armistead et al.	_702	19-	08/09/95
JR65	АН	6	1	2	8	5	8 -	2	10/03/00	Wilson et al.	-702	27-	04/30/96
7													

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None												

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183	Al	Baker <i>et al.</i> , "Protein Structure Prediction and Structural Genomics", Science, <u>294</u> :93-96 (2001)
AS .	AJ	Hess <i>et al.</i> , "Impact of Pharmacogenomics on the Clinical Laboratory", <i>Mol. Diagn.</i> , 4(4):289-98 (1999)
RS	AK	Hess <i>et al.</i> , "Gene Therapy Monitoring: Clinical Monitoring for Efficacy and Potential Toxicity, <i>Mol. Diagn.</i> , <u>2(2)</u> :147-155 (1997)

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DATE CONSIDERED

EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

USE OF COMPUTATIONALLY DERIVED PROTEIN STRUCTURES OF GENETIC

POLYMORPHISMS IN PHARMACOGENOMICS FOR DRUG DESIGN AND CLINICAL

APPLICATIONS

attachment Poper 1

FORM PTO-1449 (Modified)

ATTY. DOCKET NO. 24737-1906B

SERIAL NO. 09/704,362

LIST OF PATENTS AND PUBLICATIONS FOR PPLICANT'S INFORMATION DISCLOSURE **STATEMENT**

APPLICANT Ramnarayan et al.

FILING DATE

November 1, 2000

GROUP 1631

The Charles

U.S. PATENT DOCUMENTS

EXAMINER INITIAL			D	OCUM	IENT N	NUMB	ER		DATE	NAME	CLASS	SUB CLASS	FILING DATE
185	AA	5	7	3	6	5	0	9	04/07/98	Balaji etal.			

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None										1	l H	-CI	ニハノト

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JB.	АВ	Eisenhaber et al., "Protein structure prediction: recognition of primary, secondary, and 1600/2900 tertiary structural features from amino acid sequence", Crit. Rev. Biochem. Mol. Biol., 30:1-94, 1995									
J83	AC	de Dios <i>et al.</i> , "Secondary and Tertiary Structural Effects on Protein NMR Chemical Shifts: An ab Initio Approach", <i>Science</i> , <u>260</u> :1491-1496, 1993									
JB	AD	Dunbrack et al., "Meeting review: the Second Meeting on the Critical Assessment of Techniques for Protein Structure Prediction (CASP2), Asilomar, California, Dec. 13-16, 1996", Folding and Design, 1997, pp. R27-R42									
JB	AE	Jones, "Successful <i>ab initio</i> prediction of the teriary structure of NK-Lysin using multiple sequences and recognized supersecondary structural motifs", Proteins: Structure, function, and Genetics, Supp. 1, 1997, pp. 185-191									
JB	AF	Osguthorpe, "Improved Ab Initio Predictions with a Simplified, Flexible Geometry Model", Proteins: Structure, Function, and Genetics, Suppl. 3 (November 9, 1999), pp. 186-193									
JB	AG	Samudrala <i>et al.</i> , "Ab initio protein structure prediction using a combined hierarchical approach", Proteins: Structure, Function, and Genetics, Supp. 3, 194-198, 1999									
183	АН	Westhead and Thornton, "Protein structure prediction", <i>Curr. Opin. Biotechnol.</i> , <u>9</u> :383-389, 1998									

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DATE CONSIDERED 4/1

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